

Figure 1A
Her gulin-like Factor

1	CTCTTCTTCCTCCTCCGCTACCACCACCACACCAGAACTAGCACCAGCCCCAAATTTC	60
1	S S S S S A T T T T P E T S T S P K F H	20
61	TACGACGACATATTCCACAGAGCGATCCGAGCACTTCAAACCCCTGCCGAGACAAGGACCT	120
21	<u>T T T Y S T E R S E H F K P C R D K D L</u>	40
121	TGCATACTGTCTCAATGATGGCGAGTGCTTTGTGATCGAAACCCCTGACCGGATCCCATAA	180
41	<u>A Y C L N D G E C F V I E T L T G S H K</u>	60
181	ACACTGTCGGTGCAAAGAAGGCTACCAAGGAGTCCGTTGTGATCAATTTCTGCCGAAAAC	240
61	<u>H C R C K E G Y O G V R C D O F L P K T</u>	80
241	TGATTCCATCTTATCGGATCCAAACCACTTGGGGATTGAATTCATGGAGAGTGAAGAAGT	300
81	<u>D S I L S D P N H L G I E F M E S E E V</u>	100
301	TTATCAAAGGCAGGTGCTGTCAATTTTCATGTATCATCTTTGGAATGTTCATCGTGGGCAT	360
101	Y Q R Q V L S I S C I I F G I V I V G M	120
361	GTTCTGTGCAGCATTTCTACTTCAAAGCAAAGGAATATTACAGCAAATTTCTGTGTCTGA	420
121	F C A A F Y F K S K R N I T A N S V S E	140
421	GGAAAGATGGAAGGGTCTGCCTTCCCAGGAGCCCAATCTGCAACAAGACAAATAATGCCT	480
141	E R W K G L P S Q E P N L Q Q D K *	160
481	AACAAATGGATTAAATGATGTCTACTATTCTGCAACTTACATCTCATTTCTTTCTAATGCAT	540
541	TGGACCAGAGAAATTTAAAACTCAAATGAACTGTAAAGTTTCCCACTGACACTGTTGGG	600
601	CTAATAGTATTTCCCATGTGCAAGGCATGCATCTTTTCTTCCCCAGAGCAATGCCTCTCAT	660
661	GAGAGAGCTAATGGTATTGCAATCAGCTGCTGATTGTTTCTCTGTTCCCATTTTCTGGG	720
721	TGAAGGAAGAAAGAGCAAAAAAGTGTGTGCTTGTGAGAGAGGAGGATGGTAGATAGGCA	780
781	GAGGCAGGCTCAGAATGGAAGGACCACGTATCTTGGAAATATTACTAAGTCAGGACTTGAG	840
841	TGAAAAAAGACTAAAGGTAAGCAAATTATAAAAGGATTAGGAAACGAGTCCGGTATTG	900
901	GATATTGCTTAAAGAAAAATCCCTTATAAGTTTATACTTCCAAGACTCTGAATTGGATTA	960
961	CTGCAAACATCATTAAAGTGTTCCTAATTAAATCCCATGAGAGTAATGGAATCCTTGCTCT	1020

Figure 1B

1021	GAGACATGCACCTTACTTTTTCAGGATGATTTACCAGACTAGAACCTCCTGATTTCCCC	1080
1081	TTTTTTGTGTGTGTGAATGAACCCCTGATAAAATCTTGTGGCTGTAACATGCTCCTTAAA	1140
1141	ATGCTGATATGATAGATTTATTTTAAACAATAGGCTATAGATTAGCTGTTAGGAAGCAAA	1200
1201	TAGATTATTACAACAGGATTAAAGCAACTAAGAGTGCTAGAGATAAAAGTCTCCCAAATA	1260
1261	ATTGGAAGATAAAAGAAATATCTTAAAAAACAGAGCTACATCACACTGATATTGTAAAT	1320
1321	TCAAAATGGGTAATGAAGCTCAAAGCCTCCAAAGCTTGCAGCAAGTGCTGGTGAATTGCT	1380
1381	TGGGAAGATGCAACTAGTGTAATCTTTTACCTTTGGGTCAATGTTCTGATTCTTTTGAG	1440
1441	CTTCTGCTCACAAGACTGAGCTTGCTTGATGGTATCGGGAAGATATGAACATTTTGCGT	1500
1501	GTGCCTCCACATGCAGCCACCACAGTGTCGGTGAAGATAGCTTTTATGAACCTTCATTTA	1560
1561	CAGAGGAGGAAATGGAGGCTCAACAAGTTTAGGAAATTATTAGGGTAGCAAACTAGTGG	1620
1621	GTAGCAGAGTGGGATTCAAATCCCAGTCCCCTGTGATACAATAAGCCACGCTCTGTAGGGT	1680
1681	GCTACTGACTGGAGAAGCTCATTGCTAAGACCGCCATGTGCTCCACTGACGGCACTATC	1740
1741	TTTGTGAGAGCGTTGGAAGACAGGCAAAATTCAGGGCATGATTCTACTGGGAAAGTTG	1800
1801	TCAGAATCAAAATGGAGTCATTTGTGTTAAAAACCTGACAAATAGAGCCGAGAGAAGGAC	1860
1861	ATGAAGGGAGCAGTCACGTAGGCAAAATGCCTGATTACAAGAACTATCACAAAAGTCTGTG	1920
1921	AAAACCGCAGCTTTGCATGAAGACTATTGCAGCCTTACACGCACGAAAATAGTTCTGCAA	1980
1981	GGACATATGCCAGCAACTTCCTGTCCACCCTTGGACTGGCTCCTCCTTTCTTGGGATCC	2040
2041	TTGCAGCCAAGGATAGTGACCTCAAATCAGTTGTGTACCTAACGTTTCTGTCTTCCTAG	2100
2101	TGATAAAACATAGTTTCTTATATCGTGTGTATTCCCATTGCAACACTTATTTCCAAATAA	2160
2161	ATATTTTCTTTTAGAGTCTCAAAAAAAAAAAAAAAAAAAAAA	2199

Figure 2

Heregulin-like Factor

x

Human Heregulin

Percent Similarity: 55.782 Percent Identity: 32.653

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2 SSSSATTTPETSTSPKFHTTMYSTERSEHFKPCRDKDLAYCLNDGECFV 51
  ||.:. ....|... . .|. ||. ..|: .| :|: .:|:| |||:
149 SSESPIRISVSTEGANTSSSTSTSTGTSHLVKCAEKEKTFVCVNGGECFM 198

52 IETLTGSHKH.CRCKEGYQGVRCDFLPKTDLSILSDPNHLGIEFMESEEV 100
  :..|... :. |:|:..: | ||:..: . : | .||||| |||:|
199 VKDLSNPSRYLCKCPNEFTGDRQNYV.....MASFYKHLGIEFMEAEEL 243

101 YQRQVLSISCIIIFGIVIVGMFCAAFYFKSKRNITANSVSEERWKGLPSQE 150
  ||:..|..|..|:..:|:|:|.. | |.:. .: : :.:|.:
244 YQKRVLITIGICIALLVGIMCVVAYCKTKKQ..RKKLHDLRQSLRSER 291

151 PNLQQ 155
  |.:
292 NNMMN 296
```

Figure 3

Heregulin-like Factor

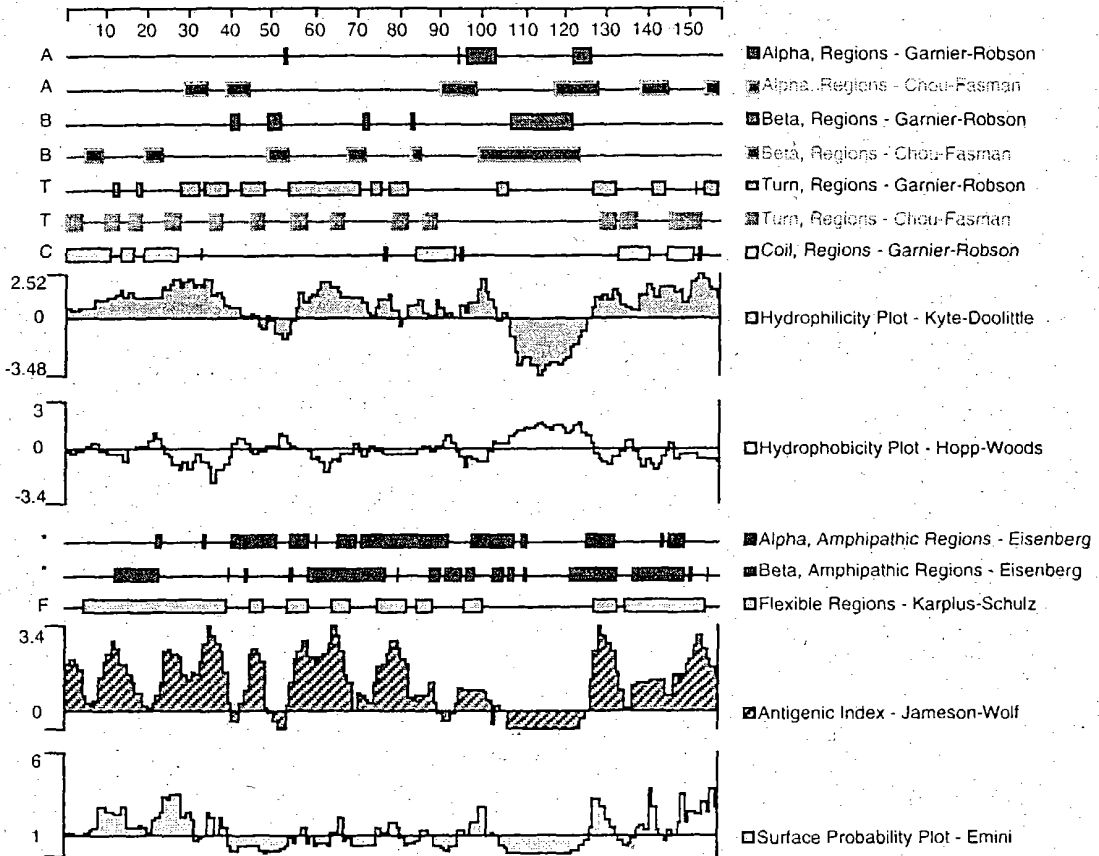


Figure 4

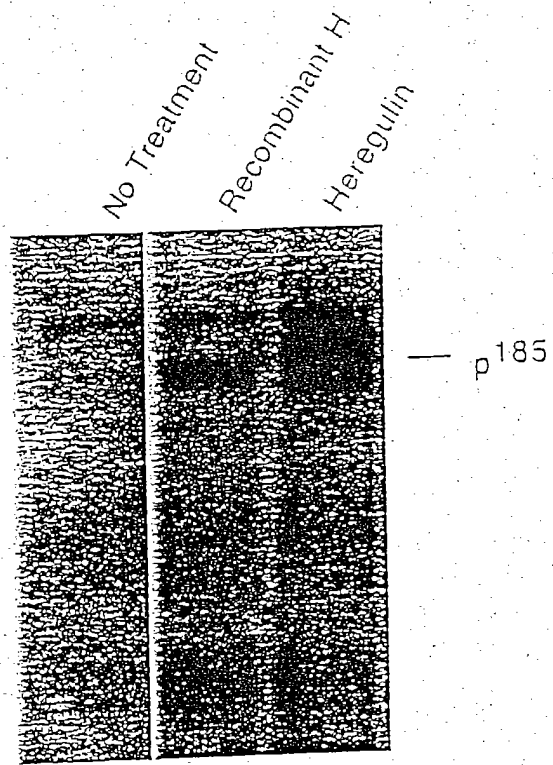


Figure 5

Amino Acid Sequences of EGF Binding Domains

	6	14	20	31	42
α TGF	SHFND	<u>C</u> PDSHTQ	<u>F</u> C FHG-TC	RFLVQEDKP---	ACV <u>C</u> HSGYVGAR <u>C</u> EHADLLA
EGF	RNSDSE	<u>C</u> PLSHDGY	<u>C</u> LHDGV	CMYIEALDKY---	ACN <u>C</u> VVGYIGER <u>C</u> OYRDLKW
HB-EGF	GKKRDP	<u>C</u> LRKYKD	<u>F</u> C IHG-E	CKYVKELRAP---	SC <u>I</u> C HPGYGGGER <u>C</u> HGLSLP
Amph	RKKKNP	<u>C</u> NAEFQ	<u>N</u> F C IHG-E	CKYIEHLEAV---	TCK <u>C</u> QOEYFGER <u>C</u> GEKSMKT
β cell	KGHFSR	<u>C</u> PKQYKH	<u>Y</u> C IKG-R	CRFVVAEQTP---	SCV <u>C</u> DEGYIGAR <u>C</u> ERVDLFY
neuR	TSHLIK	<u>C</u> AEKEKT	<u>F</u> C VNGGEC	FTVKDLSNPSRYL	<u>C</u> KCOPGFTGAR <u>C</u> TENVPMK
Hrg α 1	TSHLVK	<u>C</u> AEKEKT	<u>F</u> C VNGGEC	FMVKDLSNPSRYL	<u>C</u> KCOPGFTGAR <u>C</u> TENVPMK
Hrg β 1	TSHLVK	<u>C</u> AEKEKT	<u>F</u> C VNGGEC	FMVKDLSNPSRYL	<u>C</u> KC PNEFTGDRCQNYVMAS
HRG-2	SGHARK	<u>C</u> NETAKS	<u>Y</u> C VNGGV	CYYIEGINQLS---	CK <u>C</u> PVGYTGDR <u>C</u> QQFAMVN
HLF	SEHFKP	<u>C</u> RDKDLAY	<u>C</u> LNDGEC	FVIETLTGSHK-H	<u>C</u> RCKEGYQGVRCDOFLPKT